

Attorney Docket No. 1318

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Assistant Commissioner for Patents
Washington, D.C. 20231

**RULE 132 DECLARATION
OF
DR. STEPHEN SMITH**

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I, Stephen Smith, PhD., do hereby declare and say as follows:

1. I am skilled in the art of the field of the invention. I have a Ph.D. in Biochemical Systematics and Taxonomy of Maize and its Wild Relatives from Birmingham University. I have a M.Sc. in the Conservation and Utilization of Plant Genetic Resources from Birmingham University. I have a Bachelor of Science degree in Plant Sciences from London University. Since 1977 I have been engaged in the development, study and application of molecular markers to genetics, measuring genetic diversity and tracking pedigrees. I commenced this work at North Carolina State University as a post-doctoral research fellow. I have continued my engagement in these studies during my employment by Pioneer Hi-Bred from 1980 until the present. These studies have resulted in numerous scientific articles that have appeared in peer reviewed scientific literature.
2. This declaration is in response to the Examiner's rejection under, 35 U.S.C. § 102(e) as anticipated by or, in the alternative, under 35 U.S.C. § 103(a) as obvious over Chapman (U.S. Patent No. 6,124,530).
3. I have conducted an analysis of SSR marker data for inbred PH6JM and the

1995M 4.0415 (from www.astro.vt.edu/~sahni/sahni.html)

Appendix E

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these 78 markers, 27 were greater than 50 cM in distance, or unlinked on the genetic map.

4. Upon crossing PH6JM to any other maize line and selfing successive filial generations, one would within the realm of what is statistically possible, obtain a progeny inbred maize line that retains genetic contribution from PH6JM. Assuming that (i) the cited prior art is used as the maize line to which PH6JM is crossed, (ii) that the only difference between PH6JM and PH4TF are these 78 markers, and (iii) that all markers within a 50 cM distance will segregate together, then the odds of obtaining a PH6JM progeny inbred that is the same as PH4TF after one cycle of breeding, is 1 in 2^{27} or 1 in 134,217,728. Statistically it is extremely unlikely that a PH6JM progeny, after one cycle of breeding, would be the same as PH4TF.

5. Further, the assumptions made above vastly overstate the likelihood of breeding PH4TF from PH6JM. For example, it is common practice in quantitative genetics to determine the relation of plants by differences in markers. In doing so, one extrapolates that a percentage difference in markers is indicative of a difference in the whole genome. To assume that the only differences between PH6JM and PH4TF are for these 78 markers, when 78 markers constitute 49% of the 158 SSR loci examined, is a gross and unrealistic assumption. Further the current maize genetic map only has approximately sixty 50cM units, so by applying this limitation the maximum number of independently segregating loci one could obtain, using the most different maize lines that could ever be found, is sixty. These assumptions result in an over estimate of the odds of breeding PH4TF from PH6JM.

6. Given the difference in molecular markers between PH6JM and PH4TF, it is my expert opinion that PH6JM and PH4TF are very distinct inventions. It is also my expert opinion that, within the realm of what is statistically possible, any progeny of PH6JM developed through crossing PH6JM with another plant will be distinct from PH4TF. Given the facts and based on my education and scientific experience, I believe that the invention as claimed is not obvious nor anticipated by Chapman (U.S. Patent No. 6,124,530).

7. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements

at the United States Patent and Trademark Office may jeopardize the validity of the application or any patent issued thereon.

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Date: March 14, 2003 By: Stephen Smith
Stephen Smith